

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2052.5	76.7	418	1	AIAT_HUMAN	P01009	homo sapien
2	1909.5	71.4	409	1	AIAT_JAPAN	P01010	papio anubis
3	1508	56.4	421	1	AIAT_TIG	P50447	sus scrofa
4	1500	56.1	412	1	AIAT_CALCN	054763	calliope
5	1465.5	54.9	411	1	AIAT_RAT	P17475	ratius norv
6	1465.5	54.8	416	1	AIAT_SHEEP	P12725	ovis aries
7	1447.5	54.1	413	1	ALMM_TAMSI	054757	tamias sibi
8	1403.5	52.5	416	1	AIAT_BOVIN	P34955	bos taurus
9	1389.5	52.3	413	1	ALST_TAMSI	054759	tamias sibi
10	1389.5	52.3	413	1	ALSI_TAMSI	054760	tamias sibi
11	1387.5	51.9	413	1	ALMS_TAMSI	054761	tamias sibi
12	1347	50.4	413	1	AIIL_MOUSE	054758	tamias sibi
13	1345	50.3	413	1	AIIT_MOUSE	P07758	mus musculus
14	1341	50.1	413	1	AIT3_MOUSE	P22599	mus musculus
15	1339.5	50.1	413	1	AIAF_RABBIT	P00896	mus musculus
16	1332.5	49.8	413	1	HP55_TAMSI	P23035	oryctolagus
17	1328	49.6	413	1	AIAT_MOUSE	Q09055	tamias sibi
18	1319.5	49.3	413	1	AIAT_MOUSE	Q00897	mus musculus
19	1306	48.8	412	1	AIAT_MUSCR	P26595	mus caroli
20	1293	48.3	405	1	AIAS_CAVPO	P22325	cavia porcellus
21	1266	47.3	403	1	AIAF_CAVPO	P22324	cavia porcellus
22	1246	46.6	410	1	COTR_CAVPO	P22323	cavia porcellus
23	1165	43.6	410	1	AIAT_DIDMA	P03044	didelphis m
24	1157.5	43.3	420	1	AIAT_HUMAN	P020848	homo sapien
25	850	31.8	423	1	AACT_HUMAN	P01011	homo sapien
26	829	31.0	418	1	COTR_MOUSE	P07759	mus musculus
27	820	30.7	405	1	CBG_HUMAN	P08185	homo sapien
28	819.5	30.6	406	1	CBG_SAISC	P50451	saimiri sci
29	817.5	30.6	416	1	CPT1_RAT	P05445	r contrapsi
30	816	30.5	406	1	IPSP_HUMAN	P05154	homo sapien
31	816	30.5	418	1	CPIG_RAT	P09006	ratius norv
32	816	30.5	418	1	KAIN_HUMAN	P29622	homo sapien
33	811	30.3	383	1	CBG_RABBIT	P23775	oryctolagus

Scoring table: BUOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen Parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
AIAT_HUMAN
ID AIAT_HUMAN STANDARD; PRT; 418 AA.
AC P01009; Q9tts5; P01010; Q13672;
DT 21-JUL-1986 (Rel. 01; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antitrypsin) (PRO684/PRO229).
GN SERPINA1 OR PI OR AAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=81107980; PubMed=6319097;
RA Bollen A., Herzog A., Cravador A., Herion P., Chuchana P., Van der Straten A., Loriat R., Jacobs P., van Elsen A.; RT Cloning and expression in Escherichia coli of full-length complementary DNA coding for human alpha 1-antitrypsin.
RT DNA 255:264 (1983).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=85133645; PubMed=6387509;
RA Rosenberg S., Barr P.J., Najarian R.C., Hallewell R.A.; RT Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-antitrypsin. ";
RT Nature 312:77-80 (1984).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=85047190; PubMed=6093867;
RA Long G.L., Chandra T., Woo S.L.C., Davie E.W., Kurachi K.; RT Complete sequence of the cDNA for human alpha 1-antitrypsin and the gene for the S variant. ";
RN [4]
RN SEQUENCE FROM N.A., AND VARIANTS Z.
RX MEDLINE=87057257; PubMed=3191072;
RA Nukiwa T., Satoh K., Brantley M.L., Ogushi F., Fellis G.A., Courtney M., Crystal R.G.; RT Identification of a second mutation in the protein-coding sequence of the Z type alpha 1-antitrypsin gene. ";
RT J. Biol. Chem. 261:15389-15994 (1986).
RN [5]
RN ERRATUM.
RX MEDLINE=85116977; PubMed=2985281;
RA Courtney M., Crystal R.G.; RT J. Biol. Chem. 262:10412-10412 (1987).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=85116977; PubMed=2985281;
RA Celliberto G., Dente L., Cortese R.; RT Cell-specific expression of a transfected human alpha 1-antitrypsin gene. ";
RT Cell 41:531-540 (1985).
RN Cell 41:531-540 (1985).

[7] RN [17] RN
SEQUENCE FROM N.A.
Tissue-Fetal liver;
Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G., Zhou W., Bi J., Zhang Y., Liu M., He F.;
"Functional prediction of the coding sequences of 32 new genes deduced by analysis of cDNA clones from human fetal liver.";
submitted (DSC-1998) to the EMBL/GenBank/DBJ databases.
RN [8] RP
SEQUENCE OF 25-418.
MEDLINE=82220135; PubMed=7045697;
RA Vaughan L., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C., RT
"Structure and variation of human alpha 1-antitrypsin.";
RN [9] RP
PRELIMINARY SEQUENCE OF 25-418.
RA Chan S.K.;
RA "The covalent structure of human alphal-protease inhibitor.";
RT Fed. Proc. 41:1016-1016(1992).
RN [10] RP
SEQUENCE OF 1-67; 196-255 AND 387-418 FROM N.A.
MEDLINE=82220035; PubMed=6979715;
RA Leicht E.W., Long G.L., Chandru T., Kurachi K., Kidd V.J., Mace M. Jr., RT
Davie E.W., Woo S.L.C.;
RA "Sequence homology and structural comparison between the chromosomal human alpha 1-antitrypsin and chicken ovalbumin genes.";
RT Nature 297:655-659(1982).
RN [11] RN
SEQUENCE OF 291-418 FROM N.A.
RX RP
MEDLINE=86005469; PubMed=3876243;
RA Riley J.H., Bathurst I.C., Edbrooke M.R., Carroll R.W., Craig R.K.; RT
"Alpha 1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase and ZZ human liver.";
RN [12] RP
SEQUENCE OF 350-418 FROM N.A.
RX RP
MEDLINE=802859; PubMed=7031661;
RA Kurachi K., Chandra T., Frilezzer Degen S.J., White T.T., RT
Marchioro T.L., Woo S.L.C., Davie E.W.;
RA "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RT Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
RN [13] RN
SEQUENCE OF 387-418 FROM N.A.
RX RP
MEDLINE=85725507; PubMed=3873938;
RA Coutelle C., Speer A., Rogers J., Kalsheker N., Humphries S., RT
Williamson R.;
RT "Construction and partial characterization of a human liver cDNA library.";
RT Biomed. Acta 44:421-431(1985).
RN [14] RP
SEQUENCE OF 387-418 FROM N.A.
RX RP
MEDLINE=84292309; PubMed=6332197;
RA Loebermann H., Tokuoka R., Deisenhofer J., Huber R., RT
"Human alpha 1-proteinase inhibitor. Crystal structure analysis of two crystal modifications, molecular model and preliminary analysis of the implications for function.";
RT J. Mol. Biol. 177:531-555(1994).
RN [15] RP
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX RP
MEDLINE=89221004; PubMed=2785270;
RA Engh R., Loebermann H., Schneider M., Wiegand G., Huber R., RT
Laurell C.-B.;
RA "The S variant of human alpha 1-antitrypsin, structure and implications for function and metabolism.";
RT Protein Eng. 2:407-415(1989).
RN [16] RP
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX RP
MEDLINE=20386623; PubMed=10933492;
RA Elliott P.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
RT "Topography of a 2.0 Å structure of alpha1-antitrypsin reveals targets for rational drug design to prevent conformational disease.";
RT Protein Sci. 9:1274-1281(2000).
RN [17] RN
REVIEW;
MEDLINE=89352843; PubMed=2669992;
RX RP
Kalsheker N.; structure, function and molecular biology of alpha 1-antitrypsin: structure, function and molecular biology of the gene.;
RT RT
"Alpha 1-antitrypsin: structure, function and molecular biology of the gene.";
RL Biosci. Rep. 9:129-138(1989).
RN [18] RP
REVIEWS;
MEDLINE=91315455; PubMed=1853394;
RX RP
Wu Y., Foreman R.C.;
RT "The molecular genetics of alpha 1 antitrypsin deficiency.";
RL Bioessays 13:165-169(1991).
RN [19] RP
VARIANT M2.
MEDLINE=88324438; PubMed=2901226;
RX RP
Nukawa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F., RT
"Characterization of the gene and protein of the common alpha 1-antitrypsin normal M2 allele.";
RT RT
Am. J. Hum. Genet. 43:322-330(1988).
RN [20] RP
VARIANT M3.
MEDLINE=90368097; PubMed=2394452;
RX RP
Okayama H., Brantly M., Holmes M., Crystal R.G.;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F., RT
"Characterization of the molecular basis of the alpha 1-antitrypsin F allele.";
RT RT
Am. J. Hum. Genet. 45:1154-1158(1991).
RN [21] RP
VARIANT F.
MEDLINE=91241132; PubMed=2035534;
RX RP
Okayama H., Brantly M., Holmes M., Crystal R.G.;
RA Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.F., RT
"Characterization of the molecular basis of the alpha 1-antitrypsin F allele.";
RT RT
Am. J. Hum. Genet. 48:1154-1158(1991).
RN [22] RP
VARIANT M-HEERLEN.
MEDLINE=89154435; PubMed=2784123;
RX RP
Hofker M.H., Nukawa T., van Passen H.M.B., Nelen M., Kramps J.A., RT
RA Hofker M.H., Nukawa T., van Passen H.M.B., Nelen M., Kramps J.A., RT
"A Pro-->Leu substitution in codon 369 of the alpha-1-antitrypsin deficiency variant PI M-Heerlen.";
RT RT
Am. J. Hum. Genet. 44:894-902(1989).
RN [23] RP
VARIANT M-MALTON.
MEDLINE=9270478; PubMed=2786335;
RX RP
Fraizer G.C., Harrold T.R., Hofker M.H., Cox D.W.;
RA "In-frame single codon deletion in the M-Malton deficiency allele of alpha 1-antitrypsin.";
RT RT
Am. J. Hum. Genet. 44:264-268(1989).
RN [24] RP
VARIANT M-MINERAL SPRINGS.
MEDLINE=90097863; PubMed=1367187;
RX RP
Curiel D.T., Vogelmeier C., Hubbard R.C., Stier L.E., Cox D.W.;
RA "Molecular basis of alpha 1-antitrypsin deficiency and emphysema associated with the alpha 1-antitrypsin M-Mineral springs allele.";
RT RT
Mol. Cell. Biol. 10:47-56(1990).
RN [25] RP
VARIANT M-NICHINAN.
MEDLINE=90178096; PubMed=2309708;
RX RP
Matsuaga E., Shiokawa S., Nakamura H., Maruyama T., Tsuda K., RT
"Molecular analysis of the gene of the alpha 1-antitrypsin deficiency variant M-Nichinan.";
RT RT
Am. J. Hum. Genet. 46:602-612(1990).
RN [26] RP
VARIANT M-PROCTIDA.
MEDLINE=89008457; PubMed=3262617;
RX RP
Takahashi H., Nukawa T., Satoch K., Ogushi F., Brantly M., Fells G., RT
"Molecular analysis of the gene of the alpha 1-antitrypsin deficiency variant M-Proctida.";
RT RT
J. Biol. Chem. 263:15528-15534(1988).

Query Match	76.7%	Score 2052.5;	DB 1;	Length 418;	
Best Local Similarity	97.8%	Pred. No. 5.7e-130;			
Matches 399;	Conservative 2;	Mismatches 4;	Indels 3;	Gaps 1;	
Qy 96 GMCGRSVSPVKAMEDPOGDAQAKTIDTSHHDQDPTENKTPNLAEPAFSLYRQLAHQN 155	Db 14 GLC--CLVPVSLAEDPOGDAQAKTIDTSHHDQDPTENKTPNLAEPAFSLYRQLAHQN 70				
Qy 156 STNIFSPVSIATAFAMLSLGTKADTHBILGFLNFTIEPEAQTHGFOELLRLTNPQ 215	Db 71 STNIFSPVSIATAFAMLSLGTKADTHBILGFLNFTIEPEAQTHGFOELLRLTNPQ 130				
Qy 216 DSQLOLTGNGLFLSEGKLVDFKFLDVKLYHSEAFTHNFCDTEAKQKINDYVEKGHQ 275	Db 131 DSQLOLTGNGLFLSEGKLVDFKFLDVKLYHSEAFTHNFCDTEAKQKINDYVEKGHQ 190				
Qy 276 GKIVDLVKELDRTVFLAVLNYYFFGKWERPPEVKDTEEDFHVDQVTYKPMMKRGM 335	Db 191 GKIVDLVKELDRTVFLAVLNYYFFGKWERPPEVKDTEEDFHVDQVTYKPMMKRGM 250				
Qy 336 FNIQHCKKLISSWLLMKLGNATAIFFPDECKLQHJENELTHDITKFLENEDRSASL 395	Db 251 FNIQHCKKLISSWLLMKLGNATAIFFPDECKLQHJENELTHDITKFLENEDRSASL 310				
Qy 396 HLPKLSTGTYDLSVQLQLGTTKVFNSGADLSGVTEAPLKLKAVHLTIDEKTE 455	Db 311 HLPKLSTGTYDLSVQLQLGTTKVFNSGADLSGVTEAPLKLKAVHLTIDEKTE 370				
Qy 456 AAGAMFLEAIPMSIPPEVKENPKPFVLMIEQNTKSPLEMGVNVPTQK 503	Db 371 AAGAMFLEAIPMSIPPEVKENPKPFVLMIEQNTKSPLEMGVNVPTQK 418				
RESULT 2					
ALAT_PAPAN	STANDARD;	PRT;	409 AA.		
ID ALAT_PAPAN					
AC P01010;					
DT 21-JUL-1986 (Rel. 01, Created)					
DT 16-OCT-1996 (Rel. 01, Last sequence update)					
DT 16-OCT-2001 (Rel. 01, Last annotation update)					
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiprotease) (AAT) (Fragment).					
GN SERPINA1 OR PI.					
OS Papio anubis (Olive baboon).					
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteostomii; Cercopithecoidea; Papio.					
OX NCBI_TaxID=555;					
RN					
RP SEQUENCE FROM N.A.					
RX MEDLINE=82082539; PubMed=7031661;					
RA Kurachi K., Chandra T., Friezner Degen S.J., White T.T.,					
RA Marchioro T.L., Woo S.L.C., Davie E.W.,					
RT "Cloning and sequence of cDNA coding for alpha-1-antitrypsin.";					
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830 (1981).					
-I- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND THROMBIN.					
CC -I- SUBCELLULAR LOCATION: Extracellular.					
CC -I- TISSUE SPECIFICITY: PLASMA.					
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC DR J00321; AAA33377.1; -.					
CC DR A01248; ITBA.					
RESULT 3					
ALAT_PIG	STANDARD;	PRT;	421 AA.		
ID ALAT_PIG					
AC P5047;					
DT 01-OCT-1996 (Rel. 34, Created)					
DT 01-OCT-1996 (Rel. 34, Last sequence update)					
DT 01-NOV-1997 (Rel. 35, Last annotation update)					
DE Alpha-1-antitrypsin precursor (Alpha-1 Protease inhibitor) (Alpha-1-antiprotease).					
GN SERPINA1 OR PI.					
RN SEQUENCE FROM N.A.					
RP SEQUENCE FROM N.A.					
RC TISSUE=Liver;					
RX MEDLINE=97009792; PubMed=8856896;					
RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y., Gellin J.;					
RT Porcine alpha-1-antitrypsin (P1): cDNA sequence, polymorphism and assignment to chromosome 7q.4-q2.6.;					
RL Anim. Genet. 27:85-89 (1996).					
CC -I- FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS					

ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND THROMBIN (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: Extracellular.
 CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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CC -|- EMBL; X88780; CAA61259_1; -.
 DR HSSP; P01009; 9API.
 DR InterPro; IPR00215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN_1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Signal.

FT SIGNAL 1 24
 FT CHAIN 25 421
 FT ACT-SITE 385 386
 FT CARBOHYD 73 73
 FT CARBOHYD 110 110
 SQ SEQUENCE 421 AA: 47194 MW: 084AB2A9E600590 CRC64;

Query Match 56.4%; Score 1508; DB 1; Length 421;
 Best Local Similarity 72.0%; Pred. No. 1.3e-92;
 Matches 296; Conservative 40; Mismatches 69; Indels 6; Gaps 2;

Query	Subject	Score	Length
Qy 96	GMGKRSVSPVKAMEPDQGDAAQKTDTSHHDD--HPTFNKTKITPNAEPAFSLYRQLAH	152	152
Db 14	GLC--CLPVISLAEGLOGHAQETDYPRHIEHQHQAACRIPNLADEFSLYRQVAR	70	70
Qy 153	QSNSTNIFPSVPSVSTATAPAMSLIGTGTADTHDELEGIFNINTEIPEPQIHEGFOELLRTL	212	212
Db 71	QSNNTNIFSPVTTARAPAMSLIGTGTGATHAELEGIFNINTEKAEIHEGFOHLHTL	130	130
Qy 213	NQPSQQLQTGTGNGLFLSGLKVLDKFLDVKLYHSAFTTNGDTEEAKKQINDYVEK	272	272
Db 131	NQDPLQQLQTGTGNGLFLDEKAKLYPKFLDEKVNLYHSEAFSINFRDTEEAKKCINDYVEK	190	190
Qy 273	GTQGKIVDLYKELDRTDVFALVNYIFFKCKWERPFEVKDEEDFHVDQVTTVKVPMKMR	332	332
Db 191	GSQGKIVDLYKELDRTDVFALVNYIFFKCKWERPFEVKDEEDFHVDQVTTVKVPMKMR	250	250
Qy 333	LGMFNTQHCKKLSSWVLLMKYLNATAIIFLPDEGKLOHLENELTHDITKFLENEDRS	392	392
Db 251	LGMDLHHCOKLSSWVLLMKYLVATATAFLPDKLHQEDMLTKERAKFLKRYPS	310	310
Qy 393	ASLHPKLSTGTYDLSVQQLGIFTKVNSGADLSGVTEAPKLSKAVHKAVLTIDEK	452	452
Db 311	ANLHPKLSTGTYDLSVQQLGIFTKVNSGADLSGVTEAPKLSKAVHKAVLTIDEK	370	370
Qy 453	GTEAAGAMFLAEAPMSPIPPEVKNKEFVEMIEQNTKSPFMGKVNNPTQ	503	503
Db 371	GTEATGATILEAPMSPIPPEVKNKEFVEMIEQNTKSPFMGKVNNPTQ	421	421

Query Match 56.1%; Score 1500; DB 1; Length 412;
 Best Local Similarity 71.0%; Pred. No. 4.4e-93;
 Matches 289; Conservative 48; Mismatches 62; Indels 8; Gaps 2;

Query	Subject	Score	Length
Qy 96	GMGKSVSPVKAMEPDQGDAAQKTDTSHHDDHPTFNKTKITPNAEPAFSLYRQLAHQS	155	155
Db 14	GLC--CLPVISLAEGLOGHAQETDYPRHIEHQHQAACRIPNLADEFSLYRQVAR	70	70
Qy 216	DSQIQLITGNGLFLSEGGLVLDKFLDVKLYHSEAFTVNFGDTEAKKQINDYVEKGTQ	275	275
Db 126	NNQQLQTGTGNGLFLDQSLKFLADKFLEDVKLYHSEAFSTNFIDSEAKKQINDYVEKGTQ	185	185
Qy 336	FNQIHCKKLSSWVLLMKYLNATAIIFLPDEGKLOHLENELTHDITKFLENEDRS	395	395
Db 246	FDLLYCTTLASWVLLQMDYLNATAPFLPDEGKLOHLEPTKEILSKFLKRNHTRVNL	305	305
Qy 396	HPKLSITGTYDLSVQQLGIFTKVNSGADLSGVTEAPKLSKAVHKAVLTIDEK	455	455
Db 306	YPKLSITGTYDLSVQQLGIFTKVNSGADLSGVTEAPKLSKAVHKAVLTIDEK	365	365
Qy 456	AAGAMFLAEAPMSPIPPEVKNKEFVEMIEQNTKSPFMGKVNNPTQ	502	502
Db 366	AAGVTLAEAPMSPIPPEVKNKEFVEMIEQNTKSPFMGKVNNPTQ	412	412

RESULT 4
 A1AT_CALCN
 ID A1AT_CALCN
 AC 154763
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-1-antiproteinase Precursor (Alpha-1-antitrypsin)
 DE protease inhibitor.
 OS Callosciurus caniceps (Gray-bellied squirrel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciurinae;
 OC Callosciurus.

or send an email to license@isb-sib.ch).

CC "Expression of multiple alpha1-antitrypsin like genes in hibernating species of the squirrel family.";

CC EMBL: X15555; CA33561.1; -;

CC DR PIR: S05312; ITSH.

CC DR PIR: S01009; 1KCT.

CC DR InterPro: IPR00215; Serpin.

CC DR Pfam: PF00079; serpin_1.

CC SMART: SM0093; SERPIN_1.

CC PROSITE: PS0284; SERPIN_1.

CC DR PROSITE: PS0284; SERPIN_1.

CC KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal.

FT SIGNAL 1 24

FT CHAIN 25 416

ACT SITE 380 416 ALPHA-1-ANTITRYPSINASE.

FT CARBOHYD 68 381 REACTIVE BOND.

FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 39 39 A -> S (IN REF. 2).

FT CONFLICT 45 45 C -> A (IN REF. 2).

FT SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

FT SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 54.8%; Score 1465.5; DB 1; Length 416;

Best Local Similarity 67.6%; Pred. No. 8.9e-9;

Matches 280; Conservative 62; Mismatches 67; Indels 5; Gaps 2;

Db 7 RGLLIALLC--CLAPTSLAGLQGHAYQETDTDAQEE--AACHTIAPNANFAASIYH 61

Qy 89 RDLKCMGMGKSCVSPVAKMEDPQGDAQKDTSHHDQDHTENKTPNIAEFAFSLYR 148

Db 62 KLAHQSNNTSNIFFSPVSIATAMSLIGLTKADTHDELEGLENLNLEIPEAQIHEGFQEL 208

Qy 149 QLAHQSNNTNIFSPVSIATAMSLIGLTKADTHDELEGLENLNLEIPEAQIHEGFQEL 208

Db 62 KLAHQSNNTSNIFFSPVSIATAMSLIGAKGNTHTELLEGFLGNLTAAEATHKGFQHL 121

Qy 209 LRTLNQPSDQLQLTGNGLFLSEGKLYKHFEDVKKLYSEAFTVNGDFDEAKQIND 268

Db 122 LHTLNQPNHQQLQLTGNGLINESAKLVDLQVNTACFLPDKLNLAKFLEKK 301

Qy 269 YVEKGTOQKTYDLYKELDRTVFALVNLYFFKGKWERPEVKDTEEEFHVDQQTTVKVP 328

Db 182 YVEKGSGKTYDLYKELDRTVFALVNLYFFKGKWERPEVKDTEEEFHVDQQTTVKVP 241

Qy 329 MKRGLMFNTQHCKKLSSWVLLMKYLGNTATAIFFLPDEGKQHLENELTHDITKFLENE 388

Db 242 MNRLGMFDLYCDKLASWVLLDVTGNTVACFLPDLKSLQOLEDKLNLAKFLEKK 301

Qy 389 DRSASLHPKLSITGTYDLSVGLQLGITKVSNGADLSGYTEEAPKLKSKAYKAVL 448

Db 302 YASSANLHPKLSITGTYDLSVGLQLGITKVSNGADLSGYTEEAPKLKSKAYKAVL 361

Qy 449 IDEKGTEAAAGMFLAIPMSIPPEVKPKFVFLMEQNTKSPLFMGKVNPQTQ 502

Db 362 IDEKGTEAAAGTFILEAPMSLPPDVFNRSLFLCILYDRNTKSPLFVGKVNPQTQ 415

RESULT 7

ALMM_TAMSI STANDARD; PRT; 413 AA.

ID ALMM_TAMSI

AC 05457;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alpha-1-antitrypsin-like protein CM55-MM precursor.

OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).

OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Tamias.

OX NCBI_TaxID=64680;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=90094263; PubMed=9434174;

RC Takaihatsu N., Kojima M., Tariyama M., Ohba K., Uematsu T., Segawa C., Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.,

RT "Expression of multiple alpha1-antitrypsin like genes in hibernating species of the squirrel family.";

RT Gene 204:127-132(1997).

RL -1 - TISSUE SPECIFICITY: EXPRESSED IN LIVER.

CC -1 - SIMILARITY: BELONGS TO THE SERPIN FAMILY. HIGH, TO ALPHA-1-ANTITRYPSIN.

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CC EMBL; AB00546; BAA24416.1; -.

DR HSSP; P01095; 8AII.

DR InterPro; IPR000215; serpin.

DR Pfam; PF00079; serpin_1.

DR SMART; SM0093; SERPIN_1.

DR PROSITE; PS0284; SERPIN_1.

DR PROSITE; PS0284; SERPIN_1.

DR Serpin; Serine protease inhibitor; Glycoprotein; Signal.

KW Serpin; Serine protease inhibitor; Glycoprotein; Signal.

FT SIGNAL 1 24

FT CHAIN 25 413 ALPHA-1-ANTITRYPSIN-LIKE PROTEIN CM55-MM.

FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (POTENTIAL).

FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT ACT SITE 377 378 REACTIVE BOND (BY SIMILARITY).

SQ SEQUENCE 413 AA; 4612 MW; D1C3FB89BB20B69 CRC64;

Query Match 54.1%; Score 1447.5; DB 1; Length 413;

Best Local Similarity 68.3%; Pred. No. 1.4e-89;

Matches 274; Conservative 60; Mismatches 62; Indels 5; Gaps 1;

Db 16 SCLGFGSLAQD----AQTEASKKDQDQSPASHRIAPLAEFAESLVRLAHQSNTNIF 70

Db 71 FSPVSTATALAMSLIGTKDGTQILESDUDNLTEMAADHQFGQNLQTLNRPNTQLQ 130

Db 161 FSPVSTATAFAMSLIGTKADTHDELEGLENLNLEIPEAQIHEGFQEL 220

Qy 101 SCVSPVAKMEDPQDAAQKDTSHHDQDHTENKTPNIAEFAFSLYR 160

Db 161 FSPVSTATAFAMSLIGTKADTHDELEGLENLNLEIPEAQIHEGFQEL 220

Qy 101 SCVSPVAKMEDPQDAAQKDTSHHDQDHTENKTPNIAEFAFSLYR 160

Db 71 FSPVSTATALAMSLIGTKDGTQILESDUDNLTEMAADHQFGQNLQTLNRPNTQLQ 130

Db 221 LTGTGNCFLSEGKGLVYDVKLYKFLVEDVKSLYSEALPNTNFTTEEARQQTNSYVERGTOQIE 190

Db 131 LTSGNSLFIQNLKLLDKFLVEDVKSLYSEALPNTNFTTEEARQQTNSYVERGTOQIE 190

Db 251 CSTLSWVQLDQYDGLNQTAFLLPQKGKMHLDIVTMELSLSKFLNKTETLYDLYFPKV 310

Qy 341 CKKLSSWVLLMKYLGNTATAIFFLPDEGKQHLENELTHDITKFLENE 388

Db 311 SISGTTLKTVLHSLSGTRVSQEADLSGTYEAPKLKSKAYKAVLTDERGTTEAACM 460

Db 370 HEKGTDAAGAT 370

Qy 461 FLEAIPMSIPPEVKPKFVFLMIGLNTKSPLFMGKVNPQT 501

Db 371 FLEMIPMLPPDMKEDRPLFVYIHTKSPLFVYKVNPT 411

RESULT 8

ALAT_BOVIN STANDARD; PRT; 416 AA.

ID ALAT_BOVIN

AC P34955;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-

Mon Dec 9 12:51:04 2002

FT	CARBOHYD	266	266	N-LINKED (GLCNAC, . . .) (POTENTIAL)	CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensed@isb-sib.ch).
FT	ACT_SITE	377	378	REACTIVE BOND (BY SIMILARITY).	CC	
SQ	SEQUENCE	413 AA:	45952 MW:	430374CA26BAF08 CRC64;	CC	
Query Match		51.9%	Score 1387.5;	DB 1;	CC	
Best Local Similarity		67.0%	Pred. No 1.4e-85;	Length 413;	CC	
Matches	270;	Conservative	55;	Mismatches 73;	CC	
Qy	101	SCVSPVKAMEDPQGDAAQKTDTSHHQDQHPTENKTPNLAFFAFLSYRQLAHGSNSTNF	160		CC	
Db	16	SCLGPQGSLAQD --- AQETEAKSKDQDPQEPASHR1APHAFLAFSLYRLAROSNTNTF	70		CC	
Qy	161	FSPVSIATAFAMLSLIGTKSTKADTHDELEGALNPNLTIEPAQIHEGQELIRTLQPDSDQ	220		CC	
Db	71	FSPVSIATAALMLSLSLIGTKDQHPTQLEGQDNLTQEMAEDIHQCFQHJQTLNRPNTQ	130		CC	
Qy	221	LTTGNGLFLSEGLKLVDKLFEDLVKLYHSAFTYNGDTEAKKQINDYVERGTTQGKIVD	280		CC	
Db	131	LTSNGNLFIHONLKLDFDVKSLYHSAFTPNTNNEARQQINSYVEKGTTQGKIV	190		CC	
Qy	281	LVKELDRTVPLAVNKFVKGKQWERPKVQTEEDDFHVDQVTTVKVPMKRLGMFNTQH	340		CC	
Db	191	LVKELDSTVPLAVNKFVKGKQWLKFENBHTREDFHDEATVTPMNMREGFELHH	250		CC	
Qy	341	CKKLSWWLMLKLYGNATTAFFLPDDEGKQHLHENLDTIITKFLENEDRRSASLHHPKL	400		CC	
Db	251	CKTASLAWLQMDYLGNTATTAFFLPDDEGKQHLEDTVSTEILSFLKRNQTTTVSLPKV	310		CC	
Qy	401	SITGYDLKSYLQLGQGITKVFSNGADLSCTVTEAPLKLISKAVKAVLTIDEKTEAAGAM	460		CC	
Db	311	SISGYALKTVLSSLGCTTVFSNAADLSCTVTEAPLTVSKAHLKAVLDIDEKTEAAGAT	370		CC	
Qy	461	FLEATPMSITPEVKENPKPVFLMIEQNTKSPLEPMGKVNPTQK	503		CC	
Db	371	VGGTIFMSRKEPKIEFDRPFLVVIYEHHTKSPLEVKVYNNPTQ	413		CC	
RESULT 12						
AL1T_MOUSE	ID	AL1T_MOUSE	STANDARD;	PRTR;	413 AA.	
AC	P07788;					
DT	01-AUG-1988	(Rel. 08,	Created)			
DT	01-OCT-1996	(Rel. 34,	Last sequence update)			
DT	16-OCT-2001	(Rel. 40,	Last annotation update)			
DE	Alpha-1-antitrypsin 1-1 precursor (Serine protease inhibitor 1-1)					
DE	(Alpha-1-protease inhibitor 1) (Alpha-1-antiproteinase) (AAP).					
GN	SP1-1.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutherilia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TAXID=10090;					
RN	[1]	SEQUENCE OF 211-413 FROM N.A.				
RP	STRAIN=C57BL/6;	TISSUE=Liver;				
RP	MEDLINE=2052104;	PubMed=3007061;				
RA	Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;					
RT	"Isolation and characterization of the alpha 1-antitrypsin gene of mice."					
RT	DNA 5:29-36(1986).					
CC	-1 - FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND THROMBIN.					
CC	-1 - SIMILARITY: BELONGS TO THE SERIN FAMILY.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	CC SMART: SM0093; SERPIN; 1.					
DR	EMBL; M75721; ARCA2891; . . .					
DR	EMBL; M12586; AAA51624.1; . . .					
DR	PDB; A25495; A2495.					
DR	HSRP; P01009; 8API.					
DR	MGI; MGI:891979; 8API.					
DR	InterPro; IPR000215; Serpin.					
DR	PFam; PF00079; serpin; 1.					
DR	SMART; SM0093; SERPIN; 1.					
DR	PROSINE; P00284; SERPIN; 1.					
KW	Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal; Multigene family.					
KW	Multigene family.					
FT	SIGNAL	1	24	BY SIMILARITY;	ALPHA-1-ANTITRYPSIN 1-1.	
FT	CHAIN	25	413	REACTIVE BOND (BY SIMILARITY).		
FT	ACT_SITE	377	378	N-LINKED (GLCNAC, . . .) (POTENTIAL).		
FT	CARBONYD	64	64	N-LINKED (GLCNAC, . . .) (POTENTIAL).		
FT	CARBONYD	101	101	N-LINKED (GLCNAC, . . .) (POTENTIAL).		
FT	CARBONYD	265	265	N-LINKED (GLCNAC, . . .) (POTENTIAL).		
FT	CONFLICT	246	H	H (IN REF. 2).		
FT	CONFLICT	323	P	P -> L (IN REF. 2).		
FT	CONFLICT	404	404	L -> V (IN REF. 2).		
SQ	SEQUENCE	413 AA;	46002 MW;	1124B2C35232F4 CRC34;		
Query Match		50.4%	Score 1347;	DB 1;	Length 413;	
Best Local Similarity		62.3%	pred. No 7.3e-83;			
Matches	255;	Conservative	72;	Mismatches 72;	Indels 10;	Caps 4;
QY	96	GMCGKSKCSPVKAMDPQGDANQKTDISHDHPTEKIPNLFQDPLAFASLYRQAHOSN	155			
Db	14	GLC --CLVPSEIAED --- VQETDLSQKDS - PASHEATNLGDPATSYRELVHQS	64			
QY	156	STNIFSPVSIATAFAMLSLGKADTDEILEGLANFLNLTPEAQIHEGQELRLTNQF	215			
Db	65	TSNIFSPVSIATAFAMLSLGKADTDEILEGLANFLNLTPEAQIHEGQELRLTNQF	215			
QY	216	DSQLQTGNGLPLSEGGLVLDKFLVEVKLYHSEAFTKVQINDYVEKG	275			
Db	125	DSEQLQSTGNGLFLVNNDLKLVEKFLEAKHNYQAEEFSVNAESEAKVYNDV	244			
QY	276	GKIVDLYKELDRDTVFLAVNLYFFGKWERPFEVKDTEEDHQDQTVVKPMKRLQ	335			
Db	185	GKAAEYKKLDDQDTVFLAVNLYFFGKWERPFEVKDTEEDHQDQTVVKPMKRLQ	335			
QY	336	ENIQCKKLSSVNVLLMAGNATAFFLPDGEKQHLLENLTHDTIKLENEDRSASL	395			
Db	245	LHVHRCSTLSSVNVLLMAGNATAFFLPDGEKQHLLENLTHDTIKLENEDRSASL	395			
QY	396	HPKLSITGTGTYDLSKVGQGLGITKVFSNGADLSGTYE-APLKLSKAVLTIDE	454			
Db	395	HPRLSITGEYNLKTLMSPLGTRIFNGADLSGTEENPLKLSQAHKAVLTIDE	454			
QY	455	EAAGAMLEAIPMSIPEVKENKPFVFLMIEQNTKSPLEPMGKVNPTOK	503			
Db	365	EAAAVTVLQMVPMSPNMPILRFDHPFLFITEHTQSPFLGKVDPHK	413			
RESULT 13						
AIT2_MOUSE	ID	AIT2_MOUSE	STANDARD;	PRT;	413 AA.	
AC	P22599; Q61283;					
DT	01-APR-1990	(Rel. 14,	Created)			
DT	01-APR-1990	(Rel. 14,	Last sequence update)			
DE	Alpha-1-antitrypsin 1-2 precursor (Serine protease inhibitor 1-2).					
DE	(Alpha-1 protease inhibitor 2) (Alpha-1-antiproteinase) (AAP).					
GN	SP1-1 OR AAT2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutherilia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TAXID=10090;					
RN	[1]	SEQUENCE OF 211-413 FROM N.A.				
RP	STRAIN=C57BL/6;	TISSUE=Liver;				
RP	MEDLINE=86163765;	PubMed=3007061;				
RA	Krauter K.S., Citron B.A., Hsu M.T., Powell D., Darnell J.E. Jr.;					
RT	"Isolation and characterization of the alpha 1-antitrypsin gene of mice."					
RT	DNA 5:29-36(1986).					
CC	-1 - FUNCTION: INHIBITOR OF SERINE PROTEASES. ITS PRIMARY TARGET IS ELASTASE, BUT IT ALSO HAS A MODERATE AFFINITY FOR PLASMIN AND THROMBIN.					
CC	-1 - SIMILARITY: BELONGS TO THE SERIN FAMILY.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	CC SMART: SM0093; SERPIN; 1.					

Qy	65	STNNFSPVSIAATAFAMLSLGKTAQDTHDEILEGLNNLNLTEPAQIHEGFOELLRNQP	215
Db	65	TNNFSPVSIAATAFAMLSLGKGDHTQLEQLOFNLTQTSEADIKHSFQHLIQTLNRP	124
Qy	216	DSQQLQTGNGLFLSEAGLKLVDKFLDVKKLHYSEAFTVNGDFTEAKKQKINDYVEKGTO	275
Db	125	DSQQLSGNGLFLSEAGLKLVDKFLDVKKLHYSEAFTVNGDFTEAKKQKINDYVEKGTO	184
Qy	276	GKVLDVYKELDRTVFLAVNLTFLGKQKWERPFEYKDTEDHYDQTVTKVPMKRLGM	335
Db	185	GKAEAVKKLDQDTVFLAVNLTFLGKQKWERPFEYKDTEDHYDQTVTKVPMKRLGM	244
Qy	336	FNTQRCRKLLSSVLLMKGNGLNTAATFLPDEGKLOHLENELTHDITKFLENEDRRSASL	395
Db	245	LDWYHCSTLSSVLLMAGNATAVFLPDGKMOHLEGTLSKLISKFLKKRPRRLAQI	304
Qy	396	HLPKLSLITGTYDLSVIGLQGITKVFSNGADLSVTEE-APLKLISKAVHKAVLTIDEKG	454
Db	305	HPRLSISGENNLKLTMSPLGIGTRIFNGADLSVTEENAPLKLISQAVHKAVLTIDEKG	364
Qy	455	EAAGAMFLEAPMSIPEVKENPKPEVFLMIEQNTKSPLEMKGKVNPDK 503	
Db	365	EAATAVLLAVPYSMPPIVRDFHPLFLIEEHTQSPFLVGVVDPHK 413	
RESULT 15			
ALAF_RABBIT			
QD	ALAF_RABBIT	STANDARD;	PRT;
QD	P23035;		413 AA.
DDT	01-NOV-1991	(Rel. 20, Created)	
DDT	01-FEB-1994	(Rel. 20, Last sequence update)	
DDT	01-FEB-1994	(Rel. 28, Last annotation update)	
DDDE	Alpha-1-antiproteinase F precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor) (APF)		
DDCS	Oryctolagus cuniculus (rabbit)		
DDOC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae		
DDOC	NCBI_TaxID=9886;		
DDRN	[1]		
DDRN	SEQUENCE OF 25-41.		
DDRN	MEDLINE=91201273; PubMed=2016265;		
DDRN	Saito A., Sinohara H.;		
DDRN	"Cloning and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F; amino acid sequence comparison of alpha-1-antiproteinases of six mammals.";		
DDRN	J. Biochem. 109:158-162(1991).		
DDRN	[2]		
DDRN	SEQUENCE OF 25-41.		
DDRN	MEDLINE=86227895; PubMed=3259574;		
DDRN	Saito A., Sinohara H.;		
DDRN	"Differential interactions of rabbit plasma alpha-1-antiproteinases S		

Search completed: November 30, 2002, 12:35:38
Job time : 11 secs

Saito A., Sinohara H.;
"Amino acid sequence at the reactive site of rabbit alpha-1-
antiproteaseinase,"
J. Biochem. 108:80-85(1990).

- I - THROMBIN.
- I - SUBCELLULAR LOCATION: Extracellular.
- I - TISSUE SPECIFICITY: PLASMA.
- I - SIMILARITY: BELONGS TO THE SERPIN FAMILY.

